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SCIENCE DIRECT

Developmental Biology 295 (2006) 334 – 336

DEVELOPMENTAL BIOLOGY

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Abstracts

Postdoc Symposium

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Two hearts beat as one: Experimental compartmentalization of the Ciona heart

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The evolution of the complex, multi-chambered vertebrate heart may have involved either sub-division of the ancestral heart field or progressive addition of supplementary cardiac lineages. The single-chambered condition of the ancestral chordate heart has apparently been maintained within the tunicates, including *Ciona intestinalis*. Here, we demonstrate that specific manipulations of progenitor cell recruitment lead to compartmentalization of the *Ciona* heart. We present evidence that FGF signaling induces cardiac mesoderm within a subset of competent cells. Targeted inhibition of FGF signaling blocks heart formation, and a similar loss is obtained with a constitutive repressor form of the RTK transcriptional effector, Ets1/2 (Ets-WRPW). Conversely, targeted expression of a constitutively active form of Ets1/2, Ets-VP16, throughout the heart field doubles the number of heart progenitor cells. These excess heart cells produce an unexpected phenotype: the transformation of a one-chambered heart into a functional multi-compartment organ. These results suggest that progenitor cell recruitment was an important step during the emergence of the vertebrate multi-chambered heart. We propose that variability in the distribution of progenitor cells represents a general mechanism for potentiating evolution of novel internal structures.

doi:10.1016/j.ydbio.2006.04.040

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A systems approach to understanding N-control of gene networks in the Arabidopsis root

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We combine genomics, development and informatic approaches to gain a systems view of how nutrient sensing affects gene networks controlling plant growth, metabolic processes and development. Using a systems approach to analyze microarray data from N-treated plants, our lab has uncovered some of the first nitrogen-regulated metabolic gene networks in Arabidopsis. We are now working to use gene network analysis and cell specific gene expression studies to understand how developmental networks in roots are affected by carbon and nitrogen signaling. To uncover the networks involved in CN-control of cellular development, we are taking a 'cellomics' approach using microarray analysis of sorted root cells to identify CN-networks regulated in specific root cell types. This cellomics approach allows us to dissect gene networks in single cells, thus rendering genomics data biologically relevant for answering developmental questions. Cellomics data is analyzed in the context of an Arabidopsis 'multi-network' which integrates heterologous genomic data types, allowing the examination of mechanistic connections between both genes and proteins. Putative network nodes which act to integrate CN-signaling events and developmental pathways can then be predicted. Finally, to experimentally validate our networks, the function of putative regulatory hubs is determined by analyzing alterations to the gene network in mutants.

doi:10.1016/j.ydbio.2006.04.041

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Cdx determines the spinal cord in zebrafish by preventing rhombomere formation and inducing posterior hox gene expression in the caudal CNS

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The hindbrain and spinal cord region of the CNS arise from a common territory, the caudal neural plate; yet, the hindbrain intrinsically subdivides into rhombomeres while the spinal cord remains unsegmented. We have investigated the molecular mechanisms underlying these developmental differences in

doi:10.1016/j.ydbio.2006.04.039